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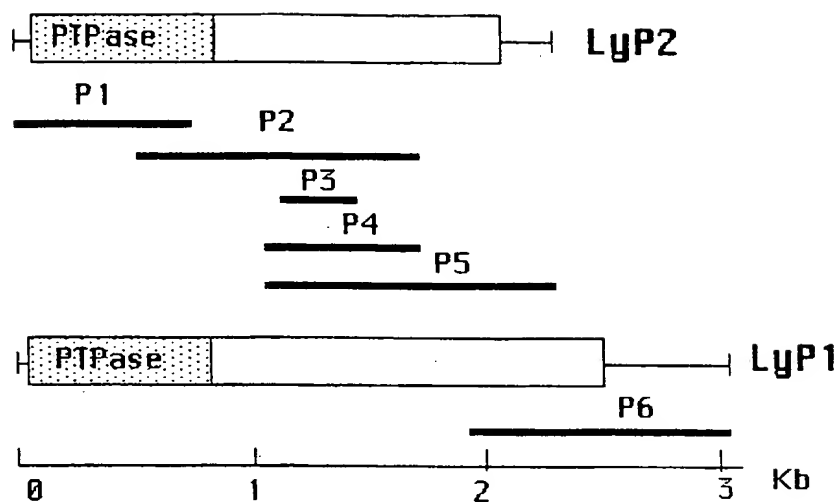


FIGURE 1

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LyP1/2	MDQREILQKF	LDEAQSCKIT	KEEFANEFLK	LKRQSTKYKA	DKTYPTTVAE	50
PEP	MDQREILQQL	LKEAQKCKLN	SEEFASEFLK	LKRQSTKYKA	DKIYPTTTVAQ	50
Consensus	MDQREILQ..	L.EAQ.KK..	.EEFA.EFLK	LKRQSTKYKA	DK.YPTTVA.	50
LyP1/2	NAKNIKKORY	KDILPYDYSR	VELSLITSDE	DSSYINANFI	KGVYGPKAYI	100
PEP	RPKNIKKORY	KDILPYDHSL	VELSLITSDE	DSSYINASFI	KGVYGPKAYI	100
Consensus	..KNIKKORY	KDILPYD.S.	VELSL.TSDE	DSSYINA.FI	KGVYGPKAYI	100
LyP1/2	ATQGPLSTTL	LDFWRMIWEY	SVLIIVMACH	EYEMGKKKCE	RYWAEPEGEMQ	150
PEP	ATQGPLSTTL	LDFWRMIWEY	RILVIIVMACH	EFEMGKKKCE	RYWAEPEGEMQ	150
Consensus	ATQGPLSTTL	LDFWRMIWEY	..L.IVMACH	E.EMGKKKCE	RYWAEPEGE.Q	150
LyP1/2	LEFGPFSVSC	EAEKRKSDYI	IRTLKVKFNS	ETRTIYQFHY	KNWPDHVDPS	200
PEP	LQFGPFSISC	EAEEKKSDYK	IRTLKAKFNN	ETRIIYQFHY	KNWPDHVDPS	200
Consensus	L.FGPFS.SC	EAEK.KSDY.	IRTLK.KFN.	ETR.IYQFHY	KNWPDHVDPS	200
LyP1/2	SIDPILELIW	DVRCYQEDDS	VPICIHCSAG	CGRTGVICAI	VDYTWMLLKD	250
PEP	SIDPILQLIW	DMRCYQEDDC	VPICIHCSAG	CGRTGVICAV	-DYTWMLLKD	249
Consensus	SIDPIL.LIW	D.RCYQEDD.	VPICIHCSAG	CGRTGVICA.	.DYTWMLLKD	250
LyP1/2	GIIPENFSVF	SLIREMRTOR	PSLVQTQEQY	ELVYNAVLEL	FKRQMDVIRD	300
PEP	GIIPKNFSVF	NLIQEMRTOR	PSLVQTQEQY	ELVYSAVLEL	FKRHMDVISD	299
Consensus	GIIP.NFSVF	.LI.EMRTOR	PSLVQTQEQY	ELVY.AVLEL	FKR.MDVI.D	300
LyP1/2	KHSGTESQAK	HCIEPEKNHTL	QADSYSPNLP	KSTTKAAKMM	NQOR---TKM	347
PEP	NHLGREIQAQ	CSIPEQSLTV	EADSCPLDLP	KNAMRDVKTT	NQHSKOGAEA	349
Consensus	.H.G.E.QA.	..IPE...T.	.ADS....LP	K.....K..	NQ.....	350
LyP1/2	EIKESSSFDF	RTSEISAKEE	LVLHPAKSST	SFDFLELNYS	FDKNADTTMK	397
PEP	ESTGGSSLGL	RTSTMNAEEE	LVLHSAKSSP	SFNCLELNCG	CNNKAVITRN	399
Consensus	E....SS...	RTS...A.EE	LVLH.AKSS.	SF...LELN..A..T..	400

FIGURE 2

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LyP1/2	WQTKAFFIVG	EPLQKHOSLD	LGSLLFEGCS	NSKPVNAAGR	YFNSKVPITR	447
PEP	GQARASPVVG	EPLQKYQSLD	FGSMLFGSCP	SALPINTADR	YHNSKGPVKR	449
Consensus	.Q..A.P.VG	EPLQK.QSLD	.GS.LF..C.	...P.N.A.R	Y.NSK.P..R	450
LyP1/2	TKSTPFELIQ	QRETKEVDSK	ENFSYLESQP	HDS-CFVEMQ	AQKVMHVSSA	496
PEP	TKSTPFELIQ	QRKTNDLAVG	DGFSCLESQ	HEHYSLELO	VORVAHVSS	499
Consensus	TKSTPFELIQ	QR.T.....	..FS.LESQ.	H.....E.Q	.Q.V.HVSS.	500
LyP1/2	ELNYSLPYDS	KHQIRNASNV	KHHDSSALGV	YSYIPLVENP	YFSSWPPSGT	546
PEP	ELNYSLPYDS	-----DASCV	PRHSPGALRV	HLTSLAEDP	YFSSSPNSA	544
Consensus	ELNYSLP...AS.V	..H...AL.V	..Y..L.E.P	YFSS.PP...	550
LyP1/2	SSKMSLDLPE	KODGTVPFSS	LLPTSSTSLF	SYNSHNSLS	LNSPTNISSL	596
PEP	DSKMSFDLPE	KODGATSPGA	LLPASSTTSF	FYSNPHDSL	MNTLTSPSP	594
Consensus	.SKMS.DLPE	KODG...P..	LLP.SST..F	.Y.N.H.SL.	.N..T..S..	600
LyP1/2	LNQESAVLAT	APRIDDEIPP	PLPVRTPESE	IVVEEAGEFS	PNVPSLSSA	646
PEP	LNQETAVEAP	SRRTDDEIPP	PLPERTPESE	IVVEEAGEPS	PRVTESE--P	642
Consensus	LNQE.AV.A.	..R.DDEIPP	PLP.RTPESE	IVVEEAGE.S	P.V..SL...	650
LyP1/2	VKVKIGTSLE	WGGTSEPCKF	DDSVILRPSK	SVKLRSPKSE	LHQDRSSPPP	696
PEP	LVVTFGASPE	CSGTSEMKS-	HDSVGFPSK	NVKLRSPKSD	RHQDGSP-PP	690
Consensus	..V..G.S.E	..GTSE.K..	.DSV...PSK	.VKLRSPKS.	.HQD.S..PP	700
LyP1	PLPERTLESF	FLADEDCMQA	QSIETYSTSY	PDTMENSTSS	KQTLKTPGKS	746
PEP	PLPERTLESF	FLADEDCIQA	QAVQTSSTSY	PETTENSTSS	KQTLRTPGKS	740
Consensus	PLPERTLESF	FLADEDC.OA	Q...T.STSY	P.T.ENSTSS	KQTL.TPGKS	750
LyP1	FTRSKSLKIL	RNMKKSICNS	CPNKPESV	QSNSSSFLN	FGFANRFSKP	796
PEP	FTRSKSLKIF	RNMKKSVCNS	SSPSKPTERV	QPKNSSSFLN	FGFGNRFSKP	790
Consensus	FTRSKSLKI.	RNMKKS.CNS	..P.KP.E.V	Q..NSSSFLN	FGF.NRFSKP	800
LyP1	KGPRNPPPTW	NI				808
PEP	KGPRNPPSAW	NM				802
Consensus	KGPRNPP..W	N.				

↓ LyP2
GKNFSWL 692

FIGURE 2 CONT'D

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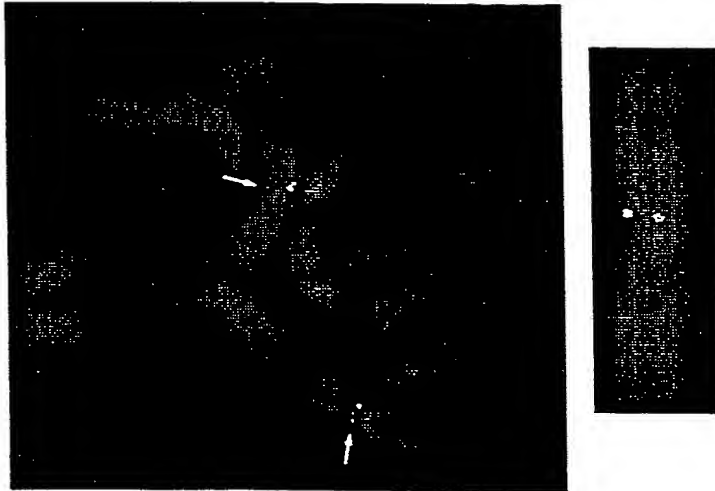


FIGURE 3A

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Chromosome 1

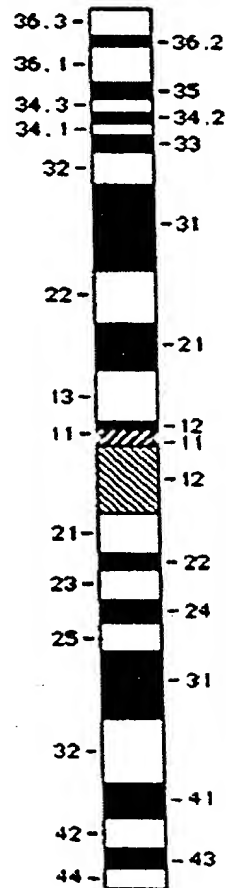


FIGURE 3B

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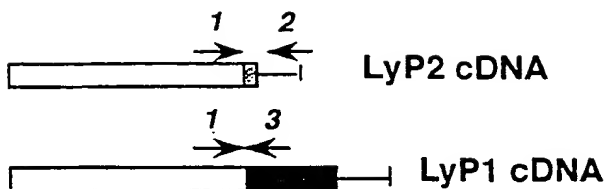
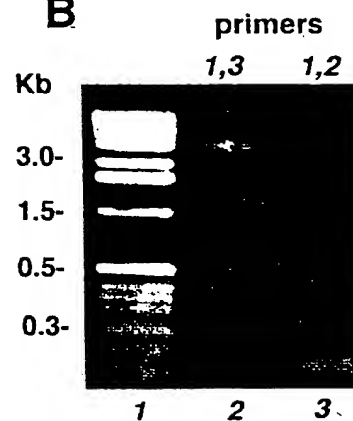
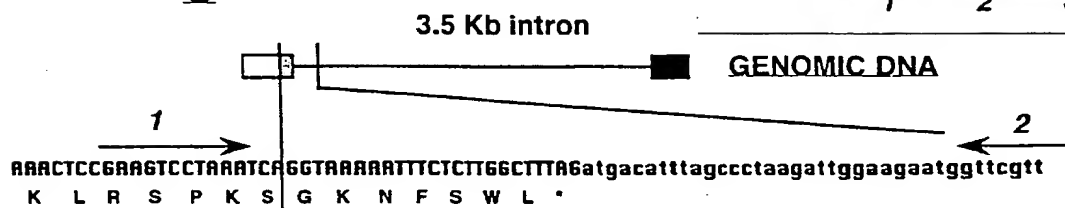
A**B****C**

FIGURE 4

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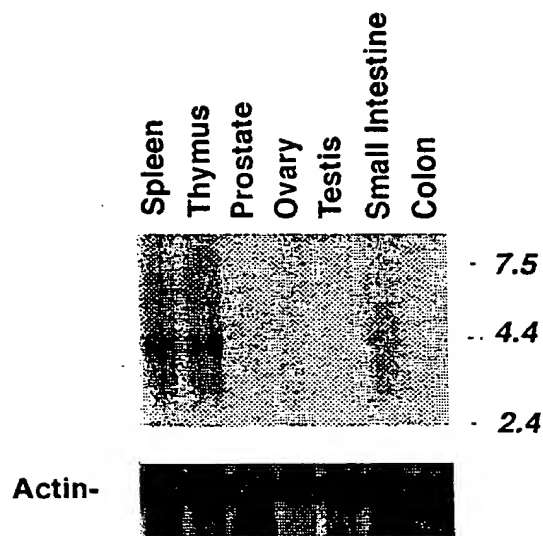


FIGURE 5A

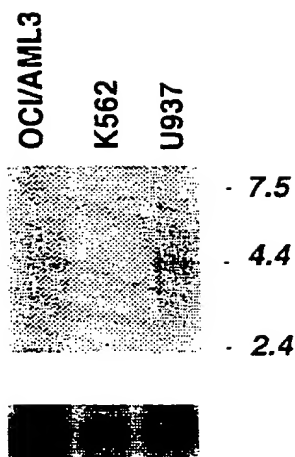


FIGURE 5B

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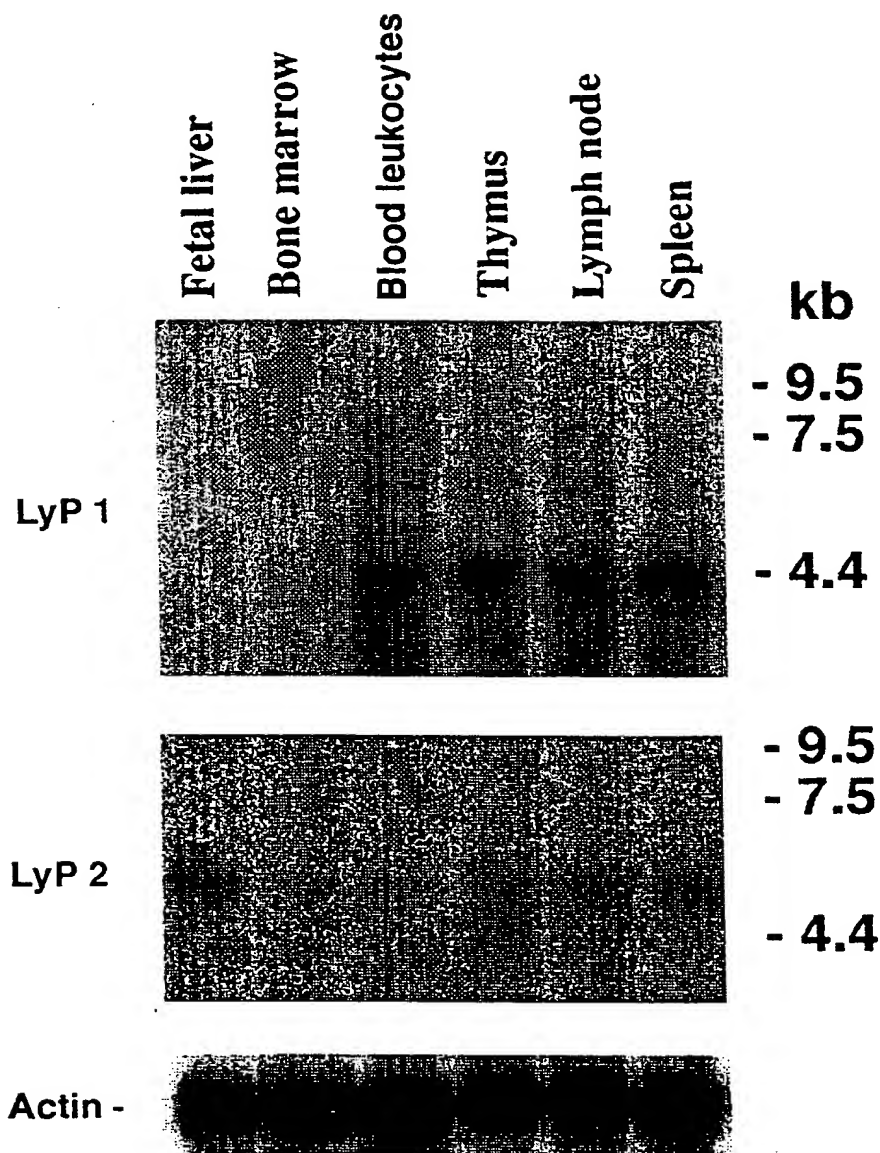


FIGURE 5C

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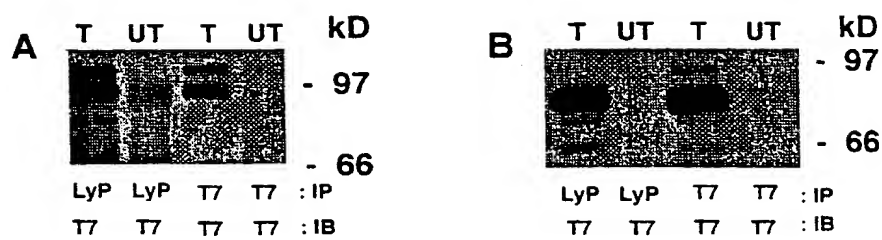


FIGURE 6

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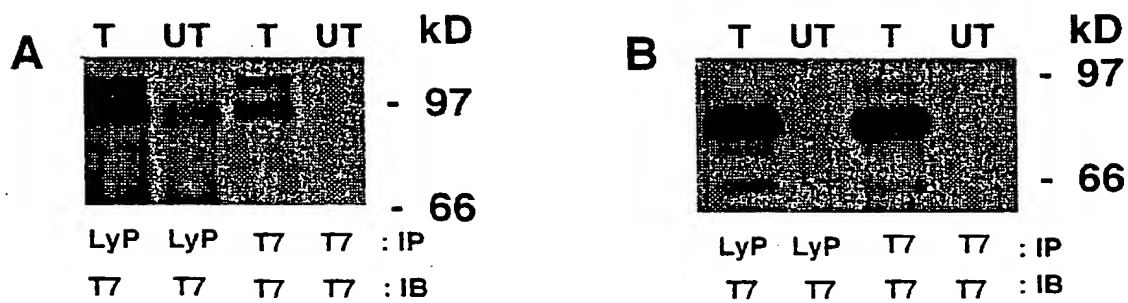


FIGURE 7

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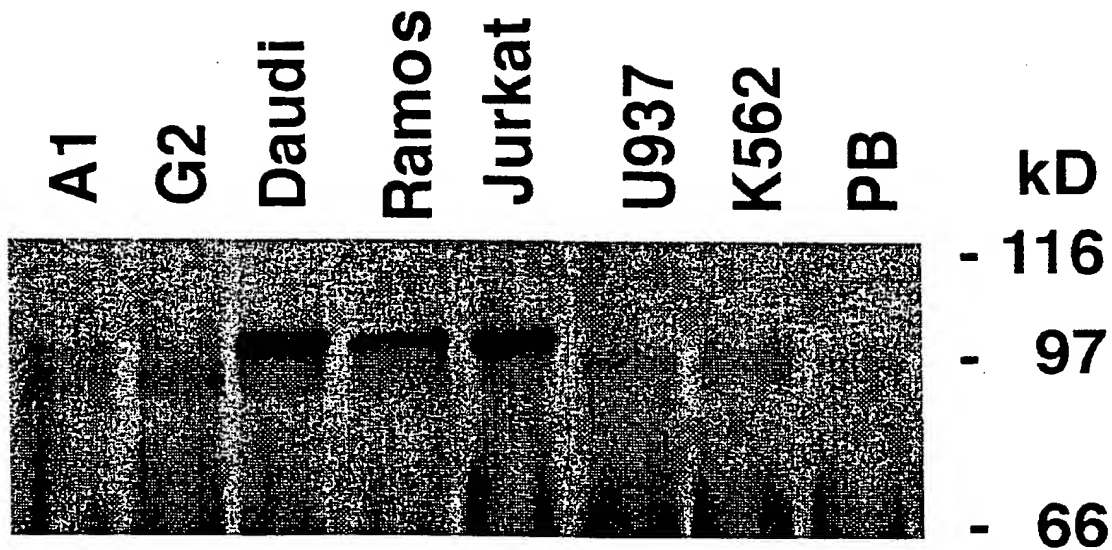


FIGURE 8

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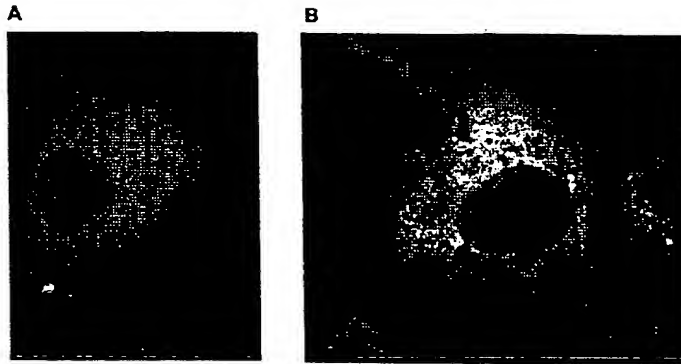


FIGURE 9

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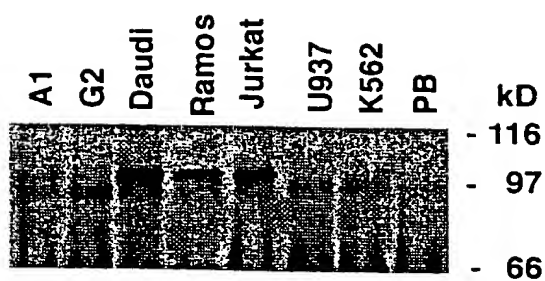


FIGURE 10

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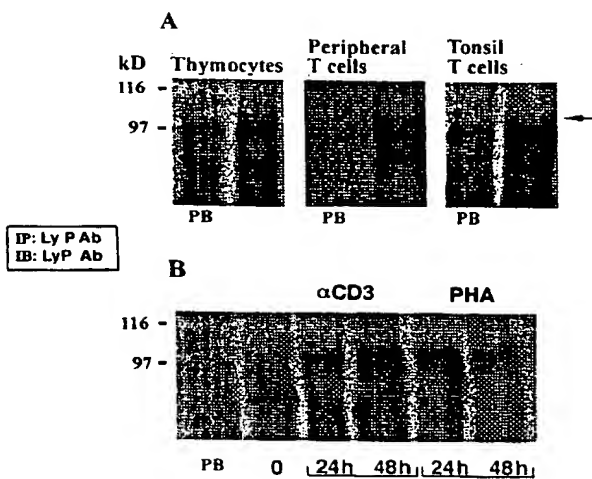


FIGURE 11

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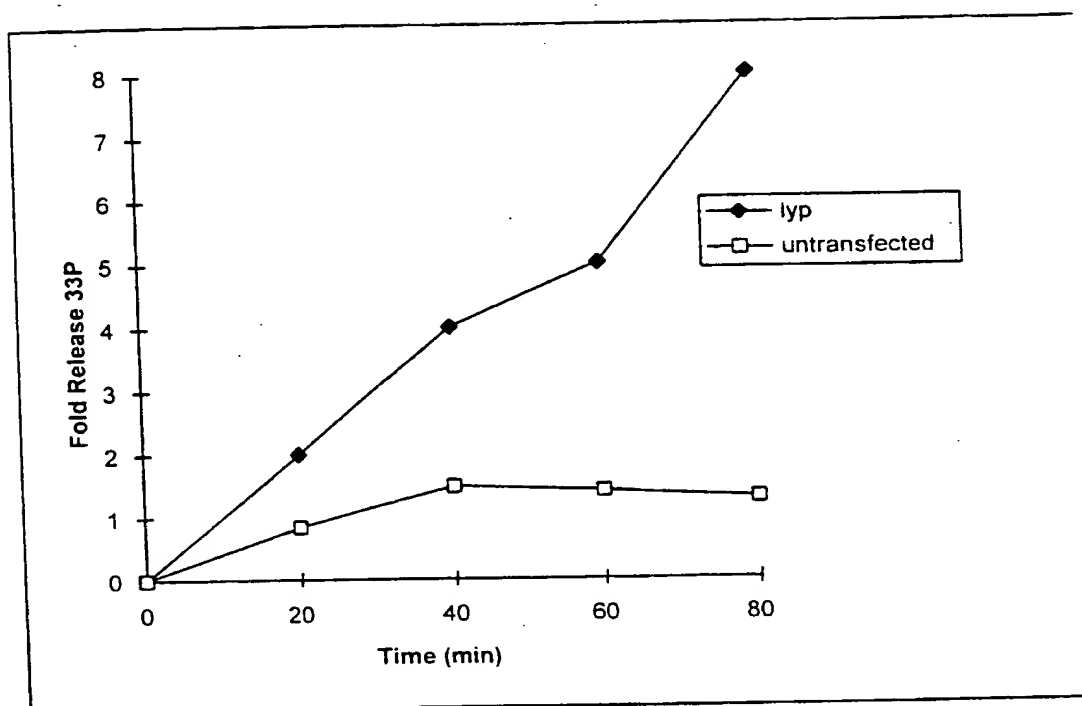


FIGURE 12

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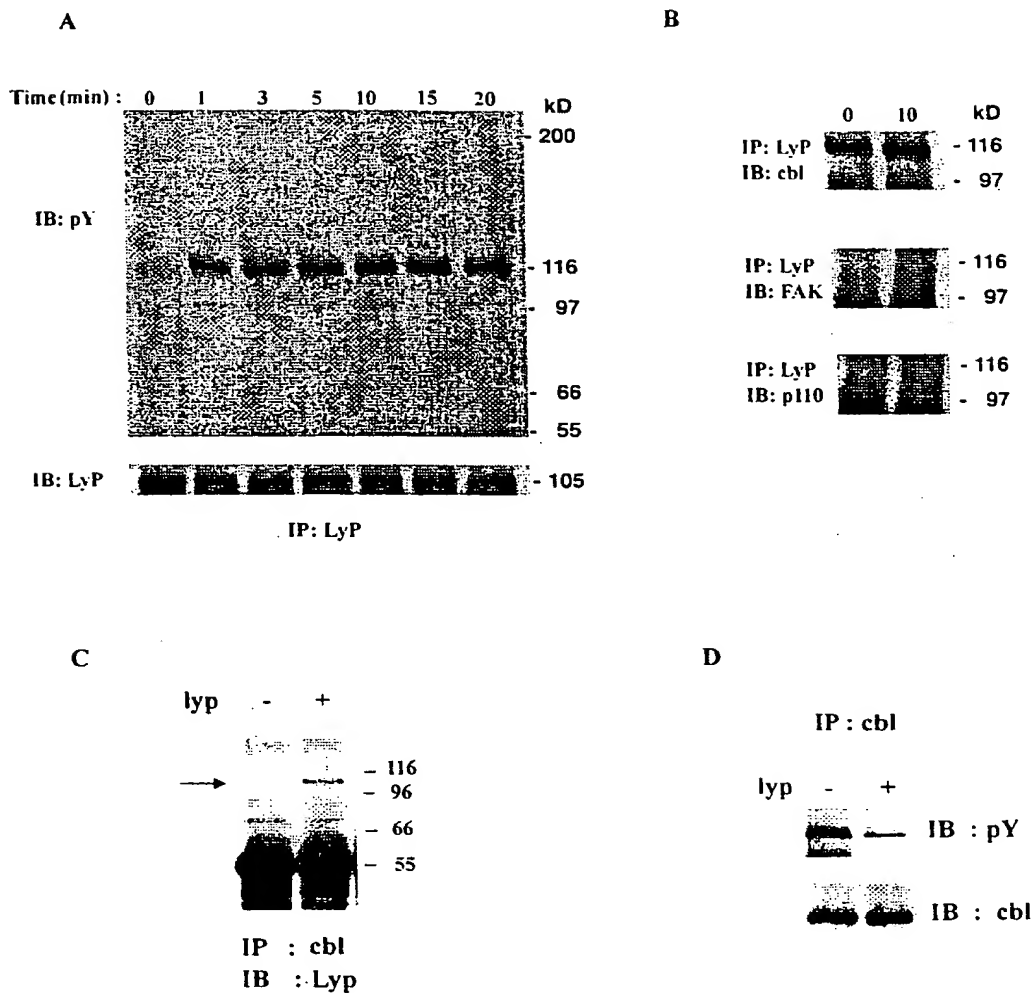


FIGURE 13

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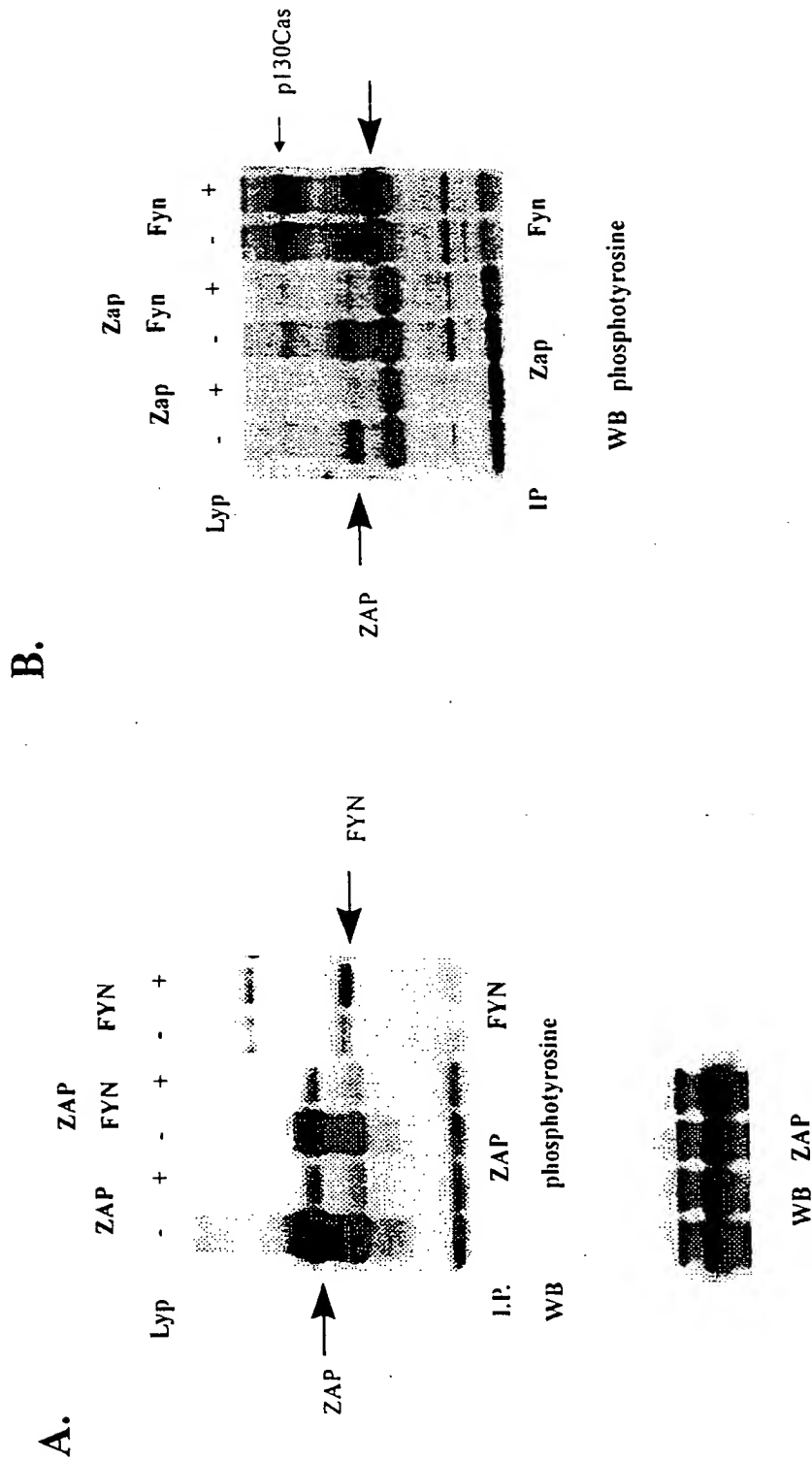
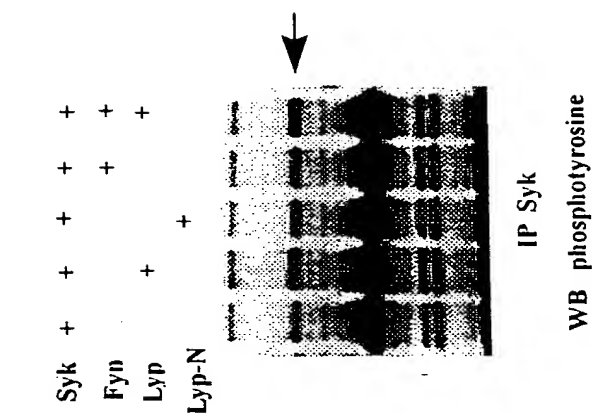


FIGURE 14

D.



C.

FIGURE 15